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Sequence Listing was accepted.

See attached Validation Report.

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217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Fri Sep 28 17:41:25 EDT 2007

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Application No: 10758524 Version No: 2.0

Input Set:

Output Set:

Started: 2007-09-14 11:27:42.124
Finished: 2007-09-14 11:27:46.606
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 482 ms
Total Warnings: 53
Total Errors: 4
No. of SeqIDs Defined: 59
Actual SeqID Count: 59

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 341	'Xaa' position not defined SEQID (8) POS (439)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)

Input Set:

Output Set:

Started: 2007-09-14 11:27:42.124
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Total Warnings: 53
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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26) This error has occurred more than 20 times, will not be displayed
E 341	'Xaa' position not defined SEQID (26) POS (502)
E 341	'Xaa' position not defined SEQID (30) POS (502)

SEQUENCE LISTING

<110> Jaworski, Jan G.
Blacklock, Brenda J.

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<130> 07148-108002

<140> 10758524

<141> 2004-01-15

<150> 09/877,476

<151> 2001-06-08

<150> 60/210,326

<151> 2000-06-08

<160> 59

<170> FastSEQ for Windows Version 4.0

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<212> DNA

<213> Arabidopsis thaliana

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Phe Phe Asn Leu Cys Leu Phe Pro Leu Thr Ala Phe Leu Ala Gly Lys	
20 25 30	

gcc tct cgg ctt acc ata aac gat ctc cac aac ttc ctt tcc tat ctc	144
Ala Ser Arg Leu Thr Ile Asn Asp Leu His Asn Phe Leu Ser Tyr Leu	
35 40 45	

caa cac aac ctt ata aca gta act tta ctc ttt gct ttc act gtt ttc	192
Gln His Asn Leu Ile Thr Val Thr Leu Leu Phe Ala Phe Thr Val Phe	
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ggg ttg gtt ctc tac atc gta acc cga ccc aat ccg gtt tat ctc gtt	240
Gly Leu Val Leu Tyr Ile Val Thr Arg Pro Asn Pro Val Tyr Leu Val	
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gac tac tcg tgt tac ctt cca cca ccg cat ctc aaa gtt agt gtc tct	288
Asp Tyr Ser Cys Tyr Leu Pro Pro Pro His Leu Lys Val Ser Val Ser	
85 90 95	

aaa gtc atg gat att ttc tac caa ata aga aaa gct gat act tct tca	336
Lys Val Met Asp Ile Phe Tyr Gln Ile Arg Lys Ala Asp Thr Ser Ser	
100 105 110	
cgg aac gtg gca tgt gat gat ccg tcc tcg ctc gat ttc ctg agg aag	384
Arg Asn Val Ala Cys Asp Asp Pro Ser Ser Leu Asp Phe Leu Arg Lys	
115 120 125	
att caa gag cgt tca ggt cta ggt gat gag acg tac agt cct gag gga	432
Ile Gln Glu Arg Ser Gly Leu Gly Asp Glu Thr Tyr Ser Pro Glu Gly	
130 135 140	
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165 170 175	
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225 230 235 240	
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245 250 255	
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Ile Tyr Ala Gly Glu Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe	
260 265 270	
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275 280 285	
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290 295 300	
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Thr Thr Leu Thr Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro	
340 345 350	
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Val Asp His Phe Cys Ile His Ala Gly Gly Arg Ala Val Ile Asp Glu	
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tca acg tta cat aga ttt ggg aat act tca tct agc tca att tgg tat	1296
Ser Thr Leu His Arg Phe Gly Asn Thr Ser Ser Ser Ser Ile Trp Tyr	
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Glu Leu Ala Tyr Ile Glu Ala Lys Gly Arg Met Lys Lys Gly Asn Lys	
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gct tgg cag att gct tta gga tca ggg ttt aag tgt aat agt gcg gtt	1392
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tgg gtg gct cta cgc aat gtc aag gca tcg gca aat agt cct tgg caa	1440
Trp Val Ala Leu Arg Asn Val Lys Ala Ser Ala Asn Ser Pro Trp Gln	
465 470 475 480	
cat tgc atc gat aga tat ccg gtt aaa att gat tct gat ttg tca aag	1488
His Cys Ile Asp Arg Tyr Pro Val Lys Ile Asp Ser Asp Leu Ser Lys	
485 490 495	
tca aag act cat gtc caa aac ggt cgg tcc taatttgatg tatctgagtg	1538
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<212> PRT

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Ile	Tyr	Ala	Gly	Glu	Asn	Arg	Ser	Met	Met	Val	Ser	Asn	Cys	Leu	Phe	
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Leu	Lys	Asp	Lys	Ile	Lys	His	Tyr	Tyr	Val	Pro	Asp	Phe	Lys	Leu	Ala	
	370					375					380					
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385					390					395					400	
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		420						425					430			
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<212> DNA

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Leu	Phe	Asn	Leu	Cys	Phe	Phe	Pro	Leu	Thr	Ala	Ile	Val	Ala	Gly	Lys	
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gcc	tat	cgg	ctt	acc	ata	gac	gat	ctt	cac	cac	tta	tac	tat	tcc	tat	144
Ala	Tyr	Arg	Leu	Thr	Ile	Asp	Asp	Leu	His	His	Leu	Tyr	Tyr	Ser	Tyr	
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Leu	Gln	His	Asn	Leu	Ile	Thr	Ile	Ala	Pro	Leu	Phe	Ala	Phe	Thr	Val	
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Val	Glu	Tyr	Ser	Cys	Tyr	Leu	Pro	Pro	Thr	His	Cys	Arg	Ser	Ser	Ile	
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tcc	aag	gtc	atg	gat	atc	ttt	tat	caa	gta	aga	aaa	gct	gat	cct	tct	336
Ser	Lys	Val	Met	Asp	Ile	Phe	Tyr	Gln	Val	Arg	Lys	Ala	Asp	Pro	Ser	
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cgg	aac	ggc	acg	tgc	gat	gac	tcg	tcg	tgg	ctt	gac	ttc	ttg	agg	aag	384
Arg	Asn	Gly	Thr	Cys	Asp	Asp	Ser	Ser	Trp	Leu	Asp	Phe	Leu	Arg	Lys	
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Ile	Gln	Glu	Arg	Ser	Gly	Leu	Gly	Asp	Glu	Thr	His	Gly	Pro	Glu	Gly	
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	165	170	175	
aac gtt aac cct aaa gat ata ggt ata ctt gtg gtg aac tca agc atg				576
Asn Val Asn Pro Lys Asp Ile Gly Ile Leu Val Val Asn Ser Ser Met				
	180	185	190	
ttt aat cca act cca tcg ctc tcc gcg atg gtc gtt aac act ttc aag				624
Phe Asn Pro Thr Pro Ser Leu Ser Ala Met Val Val Asn Thr Phe Lys				
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ctc cga agc aac gta aga agc ttt aac ctt ggt ggc atg ggt tgt agt				672
Leu Arg Ser Asn Val Arg Ser Phe Asn Leu Gly Gly Met Gly Cys Ser				
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aaa aat acg tat gct ctt gtg gtg agc aca gag aac atc act tat aac				768
Lys Asn Thr Tyr Ala Leu Val Val Ser Thr Glu Asn Ile Thr Tyr Asn				
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Ile Tyr Ala Gly Asp Asn Arg Ser Met Met Val Ser Asn Cys Leu Phe				
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Arg Val Gly Gly Ala Ala Ile Leu Leu Ser Asn Lys Pro Gly Asp Arg				
	275	280	285	
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Arg Arg Ser Lys Tyr Glu Leu Val His Thr Val Arg Thr His Thr Gly				
	290	295	300	
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Ala Asp Gly Lys Ser Phe Arg Cys Val Gln Gln Gly Asp Asp Glu Asn				
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ggc aaa atc gga gtg agt ttg tcc aag gac ata acc gat gtt gct ggt				1008
Gly Lys Ile Gly Val Ser Leu Ser Lys Asp Ile Thr Asp Val Ala Gly				
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cga acg gtt aag aaa aac ata gca acg ttg ggt ccg ttg att ctt ccg				1056
Arg Thr Val Lys Lys Asn Ile Ala Thr Leu Gly Pro Leu Ile Leu Pro				
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Leu Ser Glu Lys Leu Leu Phe Phe Val Thr Phe Met Gly Lys Lys Leu				
	355	360	365	
ttc aaa gat aaa atc aaa cat tac tac gtc ccg gat ttc aaa ctt gct				1152
Phe Lys Asp Lys Ile Lys His Tyr Tyr Val Pro Asp Phe Lys Leu Ala				
	370	375	380	

